

**AMENDMENTS TO THE SPECIFICATION**

Please delete the sequence listing from the English translation of the application and replace it with the sequence listing submitted on compact disc enclosed herewith.

In the specification at page 1, after the title and before the Field of the Invention, please insert the following:

**INCORPORATION OF SEQUENCE LISTING**

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2 REPLACEMENT 03/03/2006) and a computer-readable form of the Sequence Listing (CRF COPY REPLACEMENT 03/03/2006), all on CD-Rs, each containing: file name: Final Sequence list-12810-00057-US, date recorded: March 3, 2006, size: 307 KB.

In the specification at page 19, please replace the paragraph of sequences at lines 42-48 with the following amended paragraph:

E(V/I)GDGN(L/I)N(L/Y/F)V(F/Y) (SEQ ID NO: 72),

preferably EVGDGNLN(Y/F)V(F/Y) (SEQ ID NO: 73)

KQALPY(V/I)RC (SEQ ID NO: 74)

SWPMT(R/K)RAYF (SEQ ID NO: 75)

PEVYHFDRT (SEQ ID NO: 76)

GMRY(I/L)EPPHI (SEQ ID NO: 77)

CRLTEQVVFSVPY (SEQ ID NO: 78)

HGDLH(S/T)GS (SEQ ID NO: 79)

In the specification at page 39, please replace the paragraph of sequences at lines 14-16 with the following amended paragraph:

NLS1: N-Pro-Lys-Thr-Lys-Arg-Lys-Val-C (SEQ ID NO: 80)

NLS2: N-Pro-Lys-Lys-Lys-Arg-Lys-Val-C (SEQ ID NO: 81)

In the specification at page 39, please replace Table 1 starting at line 36 through page 42 line 45 with the following amended Table 1:

DSBI enzyme	Source organism	Recognition sequence	<u>SEQ ID NO:</u>
CRE	Bacteriophage P1	5' - AACTCTCATCGCTTCGGATAACTCCTGTTATCCGAAACAT ATCACTCACTTGGTGATTCACCGTAACTGTCTATGATTAATG - 3'	<u>82</u>
FLP	<i>Saccharomyces cerevisiae</i>	5' - GAAGTTCCATTCCGAAGTTCCATTCTAGAAAGTA TAGGAACCTTC - 3'	<u>83</u>
R	pSR1 plasmids	5' - CGAGATCATATCACTGTGGACGTTGATGAAAGAATACGTTA TTCTTTCATCAAATCGT	<u>84</u>
P-element transposase	<i>Drosophila</i>	5' - CTAGATGAAATAACATAAGGTGG	<u>85</u>
I-AniI	<i>Aspergillus nidulans</i>	5' - TTGAGGAGGTT^TCTCTGAAATAANNNNNNNNNNNNNNN 3' - AACTCCTCCAAAGAGACATTATTNNNNNNNNNNNNNN^	<u>86</u> <u>87</u>
I-DdiI	<i>Dictyostelium discoideum</i> AX3	5' - TTTTTGGTCATCCAGAAGTATAT 3' - AAAAACCA^TAGGTCTTCATATA	<u>88</u> <u>89</u>
I-CvuI	<i>Chlorella vulgaris</i>	5' - CTGGGTTCAAAACGTCGTGA^GACAGTTGG 3' - GACCCAAGTTTGCAG^CACTCTGTCAAACC	<u>90</u> <u>91</u>
I-CsmI	<i>Chlamydomonas smithii</i>	5' - GTACTAGCATGGGTCAAATGTCTTCTGG	<u>92</u>
I-CmoeI	<i>Chlamydomonas moewusii</i>	5' - TCGTAGCAGCT^CACGGTT 3' - AGCATCG^TCGAGTGCCAA	<u>93</u> <u>94</u>
I-CreI	<i>Chlamydomonas reinhardtii</i>	5' - CTGGGTTCAAAACGTCGTGA^GACAGTTGG 3' - GACCCAAGTTTGCAG^CACTCTGTCAAACC	<u>95</u> <u>96</u>
I-ChuI	<i>Chlamydomonas humicola</i>	5' - GAAGGTTGGCACCTCG^ATGTCGGCTCATC 3' - CTTCAAACCGTG^GAGCTACAGCCGAGTAG	<u>97</u> <u>98</u>
I-CpaI	<i>Chlamydomonas pallidostigmatica</i>	5' - CGATCCTAAGGTAGCGAA^ATTCA 3' - GCTAGGATTCCATC^GCTTTAAGT	<u>99</u> <u>100</u>

I-CpaII	<i>Chlamydomonas pallidostigmatica</i>	5' - CCCGGCTAACTC^TGTGCCAG 3' - GGGCCGAT^TGAGACACGGTC	<u>101</u> <u>102</u>
I-CeuI	<i>Chlamydomonas eugametos</i>	5' - CGTAACTATAACGGTCCTAA^GGTAGCGAA 3' - GCATTGATATTGCCAG^GATTCCATCGCTT	<u>103</u> <u>104</u>
I-DmoI	<i>Desulfurococcus mobilis</i>	5' - ATGCCTGCCGGTAA^GTTCCGGCGCGCAT 3' - TACGGAACGGCC^CATTCAAGGCCGCGCGTA	<u>105</u> <u>106</u>
I-SceI	<i>S.cerevisiae</i>	5' - AGTTACGCTAGGGATAA^CAGGGTAATATAG 3' - TCAATGCGATCCC^TATTGTCCCATTATATC 5' - TAGGGATAA^CAGGGTAAT 3' - ATCCC^TATTGTCCCATT ("Core" sequence)	<u>107</u> <u>108</u> <u>109</u> <u>110</u>
I-SceII	<i>S.cerevisiae</i>	5' - TTTTGATTCTTGGTCACCC^TGAAGTATA 3' - AAAACTAAGAAACCAG^TGGGACTTCATAT	<u>111</u> <u>112</u>
I-SceIII	<i>S.cerevisiae</i>	5' - ATTGGAGGTTTGGTAAC^TATTTATTACC 3' - TAACCTCCAAAACC^ATTGATAAATAATGG	<u>113</u> <u>114</u>
I-SceIV	<i>S.cerevisiae</i>	5' - TCTTTCTCTTGATTA^GCCCTAATCTACG 3' - AGAAAAGAGAAC^TAATCGGGATTAGATGC	<u>115</u> <u>116</u>
I-SceV	<i>S.cerevisiae</i>	5' - AATAATTTCT^TCTTAGTAATGCC 3' - TTATTAAAAGAAGAACATCATTA^CGG	<u>117</u> <u>118</u>
I-SceVI	<i>S.cerevisiae</i>	5' - GTTATTTAATG^TTTTAGTAGTTGG 3' - CAATAAATTACAAAATCATCA^ACC	<u>119</u> <u>120</u>
I-SceVII	<i>S.cerevisiae</i>	5' - TGTCACATTGAGGTGCACTAGTTATTAC	<u>121</u>
PI-SceI	<i>S.cerevisiae</i>	5' - ATCTATGTCGGGTGC^GGAGAAAGAGGTAAT 3' - TAGATACAGCC^CACGCCTTTCTCCATTA	<u>122</u> <u>123</u>
F-SceI	<i>S.cerevisiae</i>	5' - GATGCTGTAGGC^ATAGGCTTGGTT 3' - CTACGACA^TCCGTATCCGAACCAA	<u>124</u> <u>125</u>
F-SceII	<i>S.cerevisiae</i>	5' - CTTTCCGCAACA^GTAAAATT 3' - GAAAGGCG^TTGTCATTTAA	<u>126</u> <u>127</u>
I-HmuI	<i>Bacillus subtilis</i> bacteriophage SPO1	5' - AGTAATGAGCCTAACGCTCAGCAA 3' - TCATTACTCGGATTGC^GAGTCGTT	<u>128</u> <u>129</u>

I-HmuII	Bacillus Subtilis Bacteriophage SP82	5' - AGTAATGAGCCTAACGCTAACAAANNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNN	<u>130</u>
I-LlaI	Lactococcus lactis	5' - CACATCCATAAC^CATATCATT 3' - GTGTAGGTATTGGTATAGTAA^AAA	<u>131</u> <u>132</u>
I-MsoI	Monomastix species	5' - CTGGGTTCAAAACGTCGTGA^GACAGTTGG 3' - GACCCAAGTTTGCAG^CACTCTGTCAAACC	<u>133</u> <u>134</u>
I-NanI	Naegleria andersoni	5' - AAGTCTGGTGCCA^GCACCCGC 3' - TTCAGACC^ACGGTCGTGGCG	<u>135</u> <u>136</u>
I-NitI	Naegleria italica	5' - AAGTCTGGTGCCA^GCACCCGC 3' - TTCAGACC^ACGGTCGTGGCG	<u>137</u> <u>138</u>
I-NjaI	Naegleria jamiesoni	5' - AAGTCTGGTGCCA^GCACCCGC 3' - TTCAGACC^ACGGTCGTGGCG	<u>139</u> <u>140</u>
I-PakI	Pseudendoclo- nium akinetum	5' - CTGGGTTCAAAACGTCGTGA^GACAGTTGG 3' - GACCCAAGTTTGCAG^CACTCTGTCAAACC	<u>141</u> <u>142</u>
I-PorI	Pyrobaculum organotrophum	5' - GCGAGCCCGTAAGGGT^GTGTACGGG 3' - CGCTCGGGCATT^CCCACACATGCC	<u>143</u> <u>144</u>
I-PpoI	Physarum polycephalum	5' - TAACTATGACTCTCTAA^GGTAGCAAAT 3' - ATTGATACTGAGAG^AATTCCATCGGTTA	<u>145</u> <u>146</u>
I-ScaI	Saccharomyces capensis	5' - TGTCACATTGAGGTGCACT^AGTTATTAC 3' - ACAGTGTAACTCCAC^GTGATCAATAATG	<u>147</u> <u>148</u>
I-Ssp6803I	Synechocystis species	5' - GTCGGGCT^CATAACCCGAA 3' - CAGCCCGAGTA^TTGGGCTT	<u>149</u> <u>150</u>
PI-PfuI	Pyrococcus furiosus Vc1	5' - GAAGATGGGAGGAGGG^ACCGGACTCAACTT 3' - CTTCTACCTCTCC^TCCCTGGCCTGAGTTGAA	<u>151</u> <u>152</u>
PI-PfuII	Pyrococcus furiosus Vc1	5' - ACGAATCCATGTGGAGA^AGAGCCTCTATA 3' - TGCTTAGGTACAC^CTCTCTCGGAGATAT	<u>153</u> <u>154</u>
PI-PkoI	Pyrococcus kodakaraensis KOD1	5' - GATTTAGAT^CCCTGTACC 3' - CTAAAAA^TCTAGGGACATGG	<u>155</u> <u>156</u>

PI-PkoII	Pyrococcus kodakaraensis KOD1	5' -CAGTACTACG^GTTAC 3' -GTCATG^ATGCCAATG	<u>157</u> <u>158</u>
PI-PspI	Pyrococcus sp.	5' -AAAATCCTGGCAAACAGCTATTAT^GGGTAT 3' -TTTTAGGACCCTTGTGAT^AATACCCATA	<u>159</u> <u>160</u>
PI-TfuI	Thermococcus fumicolans ST557	5' -TAGATTTAGGT^CGCTATATCCTTCC 3' -ATCTAAAA^TCCAGCGATATAGGAAGG	<u>161</u> <u>162</u>
PI-TfuII	Thermococcus fumicolans ST557	5' -TAYGCNGAYACN^GACGGYTTYT 3' -ATRCGNCT^RTGNCTGCCRAARA	<u>163</u> <u>164</u>
PI-ThyI	Thermococcus hydrothermalis	5' -TAYGCNGAYACN^GACGGYTTYT 3' -ATRCGNCT^RTGNCTGCCRAARA	<u>165</u> <u>166</u>
PI-TliI	Thermococcus litoralis	5' -TAYGCNGAYACNGACGG^YTTYT 3' -ATRCGNCTRGN^TGCRAARA	<u>167</u> <u>168</u>
PI-TliII	Thermococcus litoralis	5' -AAATTGCTTGCAAACAGCTATTACGGCTAT	<u>169</u>
I-TevI	Bacteriophage T4	5' -AGTGGTATCAAC^GCTCAGTAGATG 3' -TCACCATAGT^TGCGAGTCATCTAC	<u>170</u> <u>171</u>
I-TevII	Bacteriophage T4	5' -GCTTATGAGTATGAAGTGAACACGT^TATTC 3' -CGAATACTCATACTTCACTTGTG^CAATAAG	<u>172</u> <u>173</u>
F-TevI	Bacteriophage T4	5' -GAAACACAAGA^AATGTTAGTAAANNNNNNNNNNNNN 3' -CTTGTGTTCTTACAAATCATTNNNNNNNNNNNN^	<u>174</u> <u>175</u>
F-TevII	Bacteriophage T4	5' -TTAATCCTCGCTTC^AGATATGGCAACTG 3' -AAATTAGGAGCGA^AGTCTATACCGTTGAC	<u>176</u> <u>177</u>

In the specification at page 76, line 1, please replace the paragraph which starts with "Fig. 9a-b:" with the following amended paragraph:

Fig. 9a-b: Sequence comparison of various 5-methylthioribose (MTR) kinases from various organisms, in particular plant organisms. Sequences from Klebsiella pneumoniae (SEQ ID NO: 40), Clostridium tetani (SEQ ID NO: 178), Arabidopsis thaliana (A. thaliana) (SEQ ID NO: 38), oilseed rape (Brassica napus) (SEQ ID NO: 64), soybean (Soy-1) (SEQ ID NO: 68), rice (Oryza sativa-1) (SEQ ID NO: 66), corn (Zea mays) (SEQ ID NO: 60), and also the consensus sequence

(Consensus) (SEQ ID NO: 179) are shown. Homologous regions can be readily deduced from the consensus sequence.